

SEQUENCE LISTING

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Toma, Salvatore
Isacchi, Antonella

<120> Tankyrase Homolog Protein (THP), Nucleic Acids, And Methods Related To The Same

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<150> 09/350,982
<151> 1999-07-09

<150> PCT/EP00/06609
<151> 2000-07-03

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<170> PatentIn version 3.1

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 Arg Asn Gly Asp Val Glu Arg Val Lys Arg Leu Val Thr Pro Glu Lys
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gtg aac agc cgc gac acg gcg ggc agg aaa tcc acc ccg ctg cac ctc
 Val Asn Ser Arg Asp Thr Ala Gly Arg Lys Ser Thr Pro Leu His Leu
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Gly Ala Asn Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His	85	90	95		
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Asn Ala Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg	100	105	110		
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His Gly Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu	115	120	125		
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His Glu Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu	130	135	140		
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Gln His Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala	145	150	155	160	
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Lys Lys Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys	180	185	190		
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Gly Arg Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val	210	215	220		
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Lys Ile Val Gln Leu Leu Gln His Gly Ala Asp Val His Ala Lys	225	230	235	240	
gat aaa ggt gat ctg gta cca tta cac aat gcc tgt tct tat ggt cat					768
Asp Lys Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His	245	250	255		
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Tyr Glu Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala	260	265	270		
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Arg Val Glu Val Cys Ser Leu Leu Ser Tyr Gly Ala Asp Pro Thr	290	295	300		
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Thr Val Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr	
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<222> (884)..(884)	
<223> The 'Xaa' at location 884 stands for Asn, Asp, His, or Tyr.	
<220>	
<223> PCR Primers	
<220>	
<221> misc_feature	
<222> (1102)..(1102)	
<223> Xaa is any amino acid	
<220>	
<221> misc_feature	

<222> (2650)..(2650)
<223> Xaa is any amino acid

<220>
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<223> Xaa is any amino acid

<400> 5

Met Ser Gly Arg Arg Cys Ala Gly Gly Ala Ala Cys Ala Ser Ala
1 5 10 15

Ala Ala Glu Ala Val Glu Pro Ala Ala Arg Glu Leu Phe Glu Ala Cys
20 25 30

Arg Asn Gly Asp Val Glu Arg Val Lys Arg Leu Val Thr Pro Glu Lys
35 40 45

Val Asn Ser Arg Asp Thr Ala Gly Arg Lys Ser Thr Pro Leu His Leu
50 55 60

Ala Ala Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn
65 70 75 80

Gly Ala Asn Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His
85 90 95

Asn Ala Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg
100 105 110

His Gly Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu
115 120 125

His Glu Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu
130 135 140

Gln His Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala
145 150 155 160

Leu Asp Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr
165 170 175

Lys Lys Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys
180 185 190

Met Met Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp
195 200 205

Gly Arg Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val
210 215 220

Lys Ile Val Gln Leu Leu Gln His Gly Ala Asp Val His Ala Lys

225

230

235

240

Asp Lys Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His
245 250 255

Tyr Glu Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala
260 265 270

Met Asp Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn
275 280 285

Arg Val Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr
290 295 300

Leu Leu Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro
305 310 315 320

Gln Leu Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu
325 330 335

Gln Ala Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser
340 345 350

Leu Glu Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Xaa
355 360 365

His Cys Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu
370 375 380

Leu Leu Leu Arg Lys Gly Ala Xaa Ile Asn Glu Lys Thr Lys Glu Phe
385 390 395 400

Leu Thr Pro Leu His Val Ala Ser Glu Lys Ala His Asn Asp Xaa Val
405 410 415

Glu Val Val Val Lys His Glu Ala Lys Val Asn Ala Leu Asp Asn Leu
420 425 430

Gly Gln Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr
435 440 445

Cys Arg Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu
450 455 460

Gln Gly Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu
465 470 475 480

Leu Gln Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu
485 490 495

Leu Glu Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys
500 505 510

Thr Val Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr
515 520 525

Pro Leu His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr
530 535 540

Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys Xaa Xaa Leu
545 550 555 560

Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu
565 570 575

Leu Leu Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys
580 585 590

Phe Thr Pro Leu His Glu Ala Ala Lys Gly Lys Tyr Glu Ile Cys
595 600 605

Lys Leu Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp
610 615 620

Gly Asn Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr Asp Ile Gln
625 630 635 640

Asp Leu Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala Ala Lys Lys Ser
645 650 655

Cys Leu Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn Val Asn Cys
660 665 670

Arg Asp Thr Gln Gly Arg His Ser Thr Pro Leu His Leu Ala Ala Gly
675 680 685

Tyr Asn Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln His Gly Ala Asp
690 695 700

Val Asn Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu His Asn Ala Ala
705 710 715 720

Ser Tyr Gly His Val Asp Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala
725 730 735

Cys Val Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro Leu His Glu Ala
740 745 750

Ala Gln Lys Gly Arg Thr Gln Leu Cys Ala Leu Xaa Leu Ala His Gly

755

760

765

Ala Asp Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr Pro Leu Asp Leu
770 775 780

Val Ser Ala Asp Asp Val Ser Ala Leu Leu Thr Ala Ala Met Pro Pro
785 790 795 800

Ser Ala Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu Asn Gly Val Arg
805 810 815

Ser Pro Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly Pro Ser Ser Pro
820 825 830

Ser Ser Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu Ser Gly Ser Phe
835 840 845

Ser Glu Leu Ser Ser Val Val Ser Ser Ser Gly Thr Glu Gly Ala Ser
850 855 860

Ser Leu Glu Lys Lys Glu Val Pro Gly Val Asp Phe Ser Ile Thr Gln
865 870 875 880

Phe Val Arg Xaa Leu Gly Leu Glu His Leu Met Asp Ile Phe Glu Arg
885 890 895

Glu Gln Ile Thr Leu Asp Val Leu Val Glu Met Gly His Lys Glu Leu
900 905 910

Lys Glu Ile Gly Ile Asn Ala Tyr Gly His Arg His Lys Leu Ile Lys
915 920 925

Gly Val Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu Asn Pro Tyr Leu
930 935 940

Thr Leu Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile Asp Leu Ser Pro
945 950 955 960

Asp Asp Lys Glu Phe Gln Ser Val Glu Glu Met Gln Ser Thr Val
965 970 975

Arg Glu His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn Arg Tyr
980 985 990

Asn Ile Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp Glu Arg
995 1000 1005

Tyr Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn His
1010 1015 1020

Ala Asn Glu Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala
1025 1030 1035

Ile Ile His Lys Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly
1040 1045 1050

Met Phe Gly Ala Gly Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser
1055 1060 1065

Asn Gln Tyr Val Tyr Gly Ile Gly Gly Gly Thr Gly Cys Pro Val
1070 1075 1080

His Lys Asp Arg Ser Cys Tyr Ile Cys His Arg Gln Leu Leu Phe
1085 1090 1095

Cys Arg Val Thr Leu Gly Lys Ser Phe Leu Gln Phe Ser Ala Met
1100 1105 1110

Lys Met Ala His Ser Pro Pro Gly His His Ser Val Thr Gly Arg
1115 1120 1125

Pro Ser Val Asn Gly Leu Ala Leu Ala Glu Tyr Val Ile Tyr Arg
1130 1135 1140

Gly Glu Gln Ala Tyr Pro Glu Tyr Leu Ile Thr Tyr Gln Ile Met
1145 1150 1155

Arg Pro Glu Gly Met Val Asp Gly
1160 1165

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<213> Artificial Sequence

<220>
<223> PCR Primers

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cccgagagct gttcgaggc

19

<210> 7
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primers

<400> 7
caatctttac tctgttatat cct

23

<210> 8

<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primers

<400> 8
aagcggccgc attatggaaa ggatcatgtc gggtcggcgc t

41

<210> 9
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primers

<400> 9
aaggatccac cataccttca ggcct

25

<210> 10
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primers

<400> 10
aaaagcttta tggaaaggat catgtcgggt cgccgctgc

39